

SEQUENCE LISTING

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<120> New Soluble and Stabilized Trimeric Form of GP41 Polypeptides

<130> 122481

<140> 10/573,704
 <141> 2006-03-27

<150> PCT/IB2004/002433
 <151> 2004-07-29

<150> 60/490,946
 <151> 2003-07-30

<160> 21

<170> PatentIn version 3.4

<210> 1
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 <212> PRT
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<220>
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Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
 1 5 10 15

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
 20 25 30

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
 35 40 45

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
 50 55 60

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
 65 70 75 80

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
 85 90 95

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
 100 105 110

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
 115 120 125

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu
 130 135 140

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Ser Gly Gly Arg Gly Gly Ser
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Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu
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Leu Gln Leu Thr Val Trp Gly
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<400> 4

Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
 1 5 10 15

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp
 20 25 30

<210> 5

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<400> 5

Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly
 1 5 10 15

Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser
 20 25 30

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<400> 6

Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr
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Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu
 20 25 30

Lys Asn Glu Gln
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attgaggcgc aacagcatct gttgcaactc acagtctggg gcatcaagca gctccaggca	120
agaatcctgg ctgtggaaag atacctaaag gatcaacagc tcctggggat tgacggtagc	180
agtggaggta gaggtggatc caatgctagt tggagtaata aatctctgga acagatttgg	240
aatcacacga cctggatgga gtgggacaga gaaattaaca attacacaag cttaatacac	300
tccttaattg aagaatcgca aaaccagcaa gaaaagaatg aacaagaatt attggaatta	360
gatctcgagc accaccacca ccaccactga	390

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<400> 8

Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn
 1 5 10 15

Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val
 20 25 30

Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr
 35 40 45

Leu Lys Asp Gln Gln Leu Leu Gly Ile Asp Gly Ser Ser Gly Gly Arg
 50 55 60

Gly Gly Ser Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu Gln Ile Trp
 65 70 75 80

Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr
 85 90 95

Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys
 100 105 110

Asn Glu Gln Glu Leu Leu Glu Leu Asp Leu Glu His His His His His
 115 120 125

His

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32

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 <212> DNA
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 <212> DNA
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 <400> 11
 ggaatccagg atccaatgct agttggagta ataaatctct ggaa 44

 <210> 12
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 agaatcctgg ctgtggaaag atacctaaag gatcaacagc tcctggggat ttggggtagc 180
 tctggaaaac tcattagcac cactgctgtg ccttggaatg ctagttggag taataaatct 240
 ctggaacaga tttggaatca cagcactgg atggagtggg acagagaaat taacaattac 300
 acaagcttaa tacactcctt aattgaagaa tcgcaaaacc agcaagaaaa gaatgaacaa 360
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 Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn
 1 5 10 15

 Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val
 20 25 30

 Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr
 35 40 45

 Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Ser Ser Gly Lys Leu
 50 55 60

 Ile Ser Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser
 65 70 75 80

 Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu
 85 90 95

 Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln
 100 105 110

 Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp
 115 120 125

 Ala Ser Leu Trp Asn Trp Phe Asn Ile
 130 135

<210> 15
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<400> 15

Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp
 1 5 10

<210> 16
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<213> Artificial Sequence

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<223> Synthetic

<400> 16

Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val
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Pro Trp Asn Ala Ser Trp Ser Asn Lys
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<210> 17

<211> 130

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<400> 17

Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn
1 5 10 15

Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val
20 25 30

Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr
35 40 45

Leu Lys Asp Gln Gln Leu Ser Gly Gly Arg Gly Gly Ser Ser Leu Glu
50 55 60

Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn
65 70 75 80

Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln
85 90 95

Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser
100 105 110

Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Asp His His His His
115 120 125

His His
130

<210> 18
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<400> 18

Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn
 1 5 10 15

Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val
 20 25 30

Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr
 35 40 45

Leu Lys Asp Gln Gln Leu Ser Gly Gly Arg Gly Gly Ser Ser Leu Glu
 50 55 60

Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn
 65 70 75 80

Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln
 85 90 95

Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser
 100 105 110

Leu Trp Asn Trp Phe Asn Ile Thr Asn Asp His His His His His His
 115 120 125

<210> 19
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<400> 19

Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn
 1 5 10 15

Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val
 20 25 30

Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr

35	40	45
Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Ser Ser Gly Gly Arg		
50	55	60
Gly Gly Ser Ser Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu		
65	70	75
Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile		
	85	90
Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu		
	100	105
Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp		
	115	120
Leu Asp His His His His His His		
130	135	
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<400> 20		
Met Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn		
1	5	10
Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val		
	20	25
Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr		
	35	40
Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Ser Ser Gly Gly Arg		
50	55	60
Gly Gly Ser Ser Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu		
65	70	75
Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile		
	85	90

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu
100 105 110

Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Asp
115 120 125

His His His His His His
130

<210> 21
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<212> PRT
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<400> 21

Met Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr
1 5 10 15

Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg
20 25 30

Tyr Leu Lys Asp Gln Gln Leu Ser Gly Gly Arg Gly Gly Ser Ser Leu
35 40 45

Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile
50 55 60

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
65 70 75 80

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
85 90 95

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Asp His His His
100 105 110

His His His
115